

## LISTAGE DES SEQUENCES

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<120> ERYTHROVIRUS HUMAIN, FRAGMENTS DUDIT VIRUS AINSI QUE LEURS APPLICATIONS

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<150> FR9715197

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 <212> DNA  
 <213> erythrovirus

<400> 73  
 TTTAAATTG TTTTCTCAC CATTAGAGTT TCA 33

<210> 74  
 <211> 725  
 <212> DNA  
 <213> erythrovirus

<400> 74  
 gaaaattatg gtagtatagc tccagatgct ttaactgtaa ctatttcaga aattgctgta 60  
 aaagatgtca cagacaaaac aggaggaggt gtgcaagtta ctgacagcac cacaggacgt 120  
 ttgtgtatgt tagtggtatca tgagtataaa taccatatg tgctagggtca gggacaagac 180  
 aactagctc cagaactgcc catttggtt tactttcccc ccagtatgc ttacttaaca 240  
 gtaggtgaag taaacacaca aggaatttca ggagacagca aaaaattggc tagtgaagaa 300  
 tcagcttttt atgtgttaga gcacagttca tttgaacttt tgggtacagg gggatctgcc 360  
 actatgtcct acaaatttcc agctgtgccc ccagaaaacc tagaaggctg cagccaacat 420  
 ttttatgaaa tgtacaaccc tttgtacggt tctcgtttag gggtagctga cacattagga 480  
 ggggacccta aatttagatc attgacacac gaagaccacg caattcagcc acaaaacttt 540  
 atgcttgggc cactaataaa ttcagtgtct accaaagaag gagacaattc taatacaggt 600  
 gctggaaaag cccttacggg gcttagtact ggcactagcc aaaacaccag aatttcccta 660  
 cgccccgggc cagtatctca gccataccat cactgggaca ctgataaata tgttacagga 720  
 ataaa 725

<210> 75  
 <211> 49  
 <212> DNA  
 <213> erythrovirus

<400> 75  
 tgccatttca catggacaaa ccacttatgg aaatgctgag gacaaagag 49

<210> 76  
 <211> 30

&lt;212&gt; DNA

&lt;213&gt; erythrovirus

&lt;400&gt; 76

tatcagcaag gggtaggaag atttccaaat 30

&lt;210&gt; 77

&lt;211&gt; 180

&lt;212&gt; DNA

&lt;213&gt; erythrovirus

&lt;400&gt; 77

gaaaaagaac agcttaagca gttacaaggt cttaacatgc acacatactt ccctaataaa 60

ggaaccaac aatacacaga ccaaattgaa cgccctctta tgggtgggctc tgtttggaac 120

agaagagctc ttcactatga aagtcagctg tggagtaaaa tccctaactt agatgacagt 180

&lt;210&gt; 78

&lt;211&gt; 64

&lt;212&gt; DNA

&lt;213&gt; erythrovirus

&lt;400&gt; 78

tttaaaactc aatttgcagc cctaggcggg tggggtttgc atcaaccacc ccctcaaata 60

tttt 64

&lt;210&gt; 79

&lt;211&gt; 152

&lt;212&gt; DNA

&lt;213&gt; erythrovirus

&lt;400&gt; 79

aggtattaaa tccatgggaa ttactacttt agttcaatat gctgtgggaa taatgacagt 60

taccatgacc tttaaattgg gacctcgaaa ggctactgga aggtggaatc cccagcctgg 120

cgtttatcct cctcatgcag ctggtcattt ac 152

&lt;210&gt; 80

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; erythrovirus

&lt;400&gt; 80

cccattgtaa acattcccca ccgtgtcctc agccaggaac cgtcacccac cgcccacctg 60

tgccgcccag attatatgtg cccctccaa taccocgtag gcaaccatct ataaaagata 120

cagacgctgt agaataaaa ttattaacta gatatgaaca acatgtaatt agaatgctaa 180

gattatgtaa tatgtacaca agtttggaag aataaaagcc tttaaataaat aattcatagt 240

gtatggttct ttaaaaattt 260

&lt;210&gt; 81

&lt;211&gt; 2013

&lt;212&gt; DNA



## &lt;213&gt; erythrovirus

&lt;400&gt; 81

atg gag cta ttt cgg ggt gtc ttg cac att tcc tct aac att ctg gac	48
Met Glu Leu Phe Arg Gly Val Leu His Ile Ser Ser Asn Ile Leu Asp	
1 5 10 15	
tgt gct aat gat aac tgg tgg tgc tct atg cta gac tta gat act tct	96
Cys Ala Asn Asp Asn Trp Trp Cys Ser Met Leu Asp Leu Asp Thr Ser	
20 25 30	
gac tgg gaa cca cta acc cat tct aac aga tta atg gca ata tat tta	144
Asp Trp Glu Pro Leu Thr His Ser Asn Arg Leu Met Ala Ile Tyr Leu	
35 40 45	
agc agt gtt gct tct aaa ctt gat ttt act ggg ggg ccg cta gca ggt	192
Ser Ser Val Ala Ser Lys Leu Asp Phe Thr Gly Gly Pro Leu Ala Gly	
50 55 60	
tgc tta tac ttt ttt cag gtg gaa tgt aac aaa ttt gag gaa ggc tat	240
Cys Leu Tyr Phe Phe Gln Val Glu Cys Asn Lys Phe Glu Glu Gly Tyr	
65 70 75 80	
cat atc cat gta gtt att ggt ggt cca gga cta aat gct aga aac tta	288
His Ile His Val Val Ile Gly Gly Pro Gly Leu Asn Ala Arg Asn Leu	
85 90 95	
act gtg tgc gta gaa ggt tta ttt aat aat gtt ctt tac cat ctt gta	336
Thr Val Cys Val Glu Gly Leu Phe Asn Asn Val Leu Tyr His Leu Val	
100 105 110	
act gaa agt gtt aaa ctt aaa ttt ttg cca ggg atg act acc aaa gga	384
Thr Glu Ser Val Lys Leu Lys Phe Leu Pro Gly Met Thr Thr Lys Gly	
115 120 125	
aaa tat ttt aga gat gga gag cag ttt ata gaa aat tac tta atg aaa	432
Lys Tyr Phe Arg Asp Gly Glu Gln Phe Ile Glu Asn Tyr Leu Met Lys	
130 135 140	
aaa att cct tta aat gtt gtg tgg tgt gta aca aat att gac ggg tat	480
Lys Ile Pro Leu Asn Val Val Trp Cys Val Thr Asn Ile Asp Gly Tyr	
145 150 155 160	
ata gac acc tgt att tcc gcc tct ttt cgg cga gga gct tgt cat gct	528
Ile Asp Thr Cys Ile Ser Ala Ser Phe Arg Arg Gly Ala Cys His Ala	
165 170 175	
aaa aga ccc cgc att act gca aat aca gac agt gct act aat gaa act	576
Lys Arg Pro Arg Ile Thr Ala Asn Thr Asp Ser Ala Thr Asn Glu Thr	
180 185 190	
ggg gag tct agc tgt gga ggg gga gat gtt gtg cca ttc gct gga aag	624
Gly Glu Ser Ser Cys Gly Gly Gly Asp Val Val Pro Phe Ala Gly Lys	
195 200 205	
gga aca aaa gcg ggg tta aag ttt caa acc atg gta aat tgg cta tgt	672
Gly Thr Lys Ala Gly Leu Lys Phe Gln Thr Met Val Asn Trp Leu Cys	
210 215 220	

gaa Glu 225	aac Asn	aga Arg	gta Val	ttt Phe	act Thr	gaa Glu	gat Asp	aaa Lys	tgg Trp	aaa Lys	tta Leu	gtg Val	gat Asp	ttt Phe	aac Asn	720
caa Gln	tat Tyr	act Thr	tta Leu	tta Leu	agt Ser	agc Ser	agt Ser	cac His	agt Ser	ggc Gly	agc Ser	ttt Phe	caa Gln	att Ile	caa Gln	768
agt Ser	gcc Ala	tta Leu	aag Lys	tta Leu	gct Ala	att Ile	tat Tyr	aaa Lys	gct Ala	act Thr	aac Asn	tta Leu	gta Val	ccc Pro	act Thr	816
agt Ser	aca Thr	ttc Phe	ttg Leu	tta Leu	cat His	tca Ser	gac Asp	ttt Phe	gag Glu	cag Gln	gtt Val	act Thr	tgc Cys	att Ile	aaa Lys	864
gaa Glu	aat Asn	aaa Lys	ata Ile	gta Val	aaa Lys	tta Leu	tta Leu	ttg Leu	tgt Cys	caa Gln	aac Asn	tat Tyr	gat Asp	cct Pro	ctt Leu	912
tta Leu	gtg Val	ggg Gly	caa Gln	cat His	gtg Val	tta Leu	agg Arg	tgg Trp	att Ile	gac Asp	aaa Lys	aaa Lys	tgt Cys	ggg Gly	aaa Lys	960
aaa Lys	aac Asn	acc Thr	ctg Leu	tgg Trp	ttt Phe	tac Tyr	ggg Gly	cca Pro	cca Pro	agt Ser	act Thr	gga Gly	aaa Lys	aca Thr	aat Asn	1008
ttg Leu	gca Ala	atg Met	gct Ala	att Ile	gct Ala	aaa Lys	act Thr	gta Val	cca Pro	gtg Val	tat Tyr	gga Gly	atg Met	gtg Val	aat Asn	1056
tgg Trp	aat Asn	aat Asn	gaa Glu	aac Asn	ttt Phe	cca Pro	ttt Phe	aat Asn	gat Asp	gta Val	gcg Ala	ggg Gly	aaa Lys	agt Ser	ttg Leu	1104
gtg Val	gtc Val	tgg Trp	gat Asp	gaa Glu	ggc Gly	att Ile	att Ile	aag Lys	tcc Ser	act Thr	att Ile	gtg Val	gaa Glu	gct Ala	gca Ala	1152
aaa Lys	gcc Ala	att Ile	tta Leu	ggg Gly	ggg Gly	cag Gln	cca Pro	acc Thr	agg Arg	gta Val	gat Asp	cag Gln	aaa Lys	atg Met	cgt Arg	1200
ggc Gly	agt Ser	gtg Val	gca Ala	gtg Val	ccc Pro	ggg Gly	gtg Val	cct Pro	gtg Val	gtt Val	ata Ile	acc Thr	agc Ser	aat Asn	ggg Gly	1248
gac Asp	att Ile	aca Thr	ttt Phe	gtt Val	gtg Val	agt Ser	ggg Gly	aat Asn	acc Thr	act Thr	aca Thr	act Thr	gtg Val	cat His	gct Ala	1296
aaa Lys	gcc Ala	tta Leu	aag Lys	gaa Glu	cgg Arg	atg Met	gta Val	aag Lys	cta Leu	aac Asn	ttt Phe	acc Thr	ata Ile	aga Arg	tgt Cys	1344
agc Ser	cct Pro	gac Asp	atg Met	ggg Gly	tta Leu	ctt Leu	aca Thr	gag Glu	gct Ala	gat Asp	gta Val	caa Gln	caa Gln	tgg Trp	cta Leu	1392

act tgg tgt aat gca caa agc tgg agc cac tat gaa aac tgg gca ata	1440
Thr Trp Cys Asn Ala Gln Ser Trp Ser His Tyr Glu Asn Trp Ala Ile	
465 470 475 480	
aac tac aca ttt gat ttc cct gga ata aat gca gat gcc ctc cac cca	1488
Asn Tyr Thr Phe Asp Phe Pro Gly Ile Asn Ala Asp Ala Leu His Pro	
485 490 495	
gat ctc caa acc acc ccc att gtc cca gac acc agt atc agc agc agt	1536
Asp Leu Gln Thr Thr Pro Ile Val Pro Asp Thr Ser Ile Ser Ser Ser	
500 505 510	
ggg ggt gaa agc tct gaa gaa ctc agt gaa agc agc ttt ttc aac ctc	1584
Gly Gly Glu Ser Ser Glu Glu Leu Ser Glu Ser Ser Phe Phe Asn Leu	
515 520 525	
atc act cca ggc gcc tgg aac agt gaa acc ccg cgc tct agt acg ccc	1632
Ile Thr Pro Gly Ala Trp Asn Ser Glu Thr Pro Arg Ser Ser Thr Pro	
530 535 540	
gtc ccc ggg acc agt tca gga gaa tca ttt gtc gga agc cca gtt tcc	1680
Val Pro Gly Thr Ser Ser Gly Glu Ser Phe Val Gly Ser Pro Val Ser	
545 550 555 560	
tcc gaa gtg gta gcc gcg tcg tgg gag gaa gct ttt tac acg ccg ctt	1728
Ser Glu Val Val Ala Ala Ser Trp Glu Glu Ala Phe Tyr Thr Pro Leu	
565 570 575	
gcc gat cag ttt cgt gaa ctg tta gta ggg gtt gac ttt gta tgg gat	1776
Ala Asp Gln Phe Arg Glu Leu Leu Val Gly Val Asp Phe Val Trp Asp	
580 585 590	
ggg ggt gga ttg cct gtt tgc tgt gtg gaa cat ata aac aac agt	1824
Gly Val Arg Gly Leu Pro Val Cys Cys Val Glu His Ile Asn Asn Ser	
595 600 605	
ggg gga ggg ttg ggg ctt tgc cct cat tgt att aat gtg gga gct tgg	1872
Gly Gly Gly Leu Gly Leu Cys Pro His Cys Ile Asn Val Gly Ala Trp	
610 615 620	
tat aat gga tgg aaa ttt aga gag ttt act cca gac tta gtg cgc tgc	1920
Tyr Asn Gly Trp Lys Phe Arg Glu Phe Thr Pro Asp Leu Val Arg Cys	
625 630 635 640	
agt tgt cat gta gga gcc tct aac cca ttt tct gtg tta act tgt aaa	1968
Ser Cys His Val Gly Ala Ser Asn Pro Phe Ser Val Leu Thr Cys Lys	
645 650 655	
aaa tgt gct tac ctg tct gga tta caa agt ttt gta gat tat gag	2013
Lys Cys Ala Tyr Leu Ser Gly Leu Gln Ser Phe Val Asp Tyr Glu	
660 665 670	
<210> 82	
<211> 671	
<212> PRT	
<213> erythrovirus	
<400> 82	

Met	Glu	Leu	Phe	Arg	Gly	Val	Leu	His	Ile	Ser	Ser	Asn	Ile	Leu	Asp	1	5	10	15
Cys	Ala	Asn	Asp	Asn	Trp	Trp	Cys	Ser	Met	Leu	Asp	Leu	Asp	Thr	Ser	20	25	30	
Asp	Trp	Glu	Pro	Leu	Thr	His	Ser	Asn	Arg	Leu	Met	Ala	Ile	Tyr	Leu	35	40	45	
Ser	Ser	Val	Ala	Ser	Lys	Leu	Asp	Phe	Thr	Gly	Gly	Pro	Leu	Ala	Gly	50	55	60	
Cys	Leu	Tyr	Phe	Phe	Gln	Val	Glu	Cys	Asn	Lys	Phe	Glu	Glu	Gly	Tyr	65	70	75	80
His	Ile	His	Val	Val	Ile	Gly	Gly	Pro	Gly	Leu	Asn	Ala	Arg	Asn	Leu	85	90	95	
Thr	Val	Cys	Val	Glu	Gly	Leu	Phe	Asn	Asn	Val	Leu	Tyr	His	Leu	Val	100	105	110	
Thr	Glu	Ser	Val	Lys	Leu	Lys	Phe	Leu	Pro	Gly	Met	Thr	Thr	Lys	Gly	115	120	125	
Lys	Tyr	Phe	Arg	Asp	Gly	Glu	Gln	Phe	Ile	Glu	Asn	Tyr	Leu	Met	Lys	130	135	140	
Lys	Ile	Pro	Leu	Asn	Val	Val	Trp	Cys	Val	Thr	Asn	Ile	Asp	Gly	Tyr	145	150	155	160
Ile	Asp	Thr	Cys	Ile	Ser	Ala	Ser	Phe	Arg	Arg	Gly	Ala	Cys	His	Ala	165	170	175	
Lys	Arg	Pro	Arg	Ile	Thr	Ala	Asn	Thr	Asp	Ser	Ala	Thr	Asn	Glu	Thr	180	185	190	
Gly	Glu	Ser	Ser	Cys	Gly	Gly	Gly	Asp	Val	Val	Pro	Phe	Ala	Gly	Lys	195	200	205	
Gly	Thr	Lys	Ala	Gly	Leu	Lys	Phe	Gln	Thr	Met	Val	Asn	Trp	Leu	Cys	210	215	220	
Glu	Asn	Arg	Val	Phe	Thr	Glu	Asp	Lys	Trp	Lys	Leu	Val	Asp	Phe	Asn	225	230	235	240
Gln	Tyr	Thr	Leu	Leu	Ser	Ser	Ser	His	Ser	Gly	Ser	Phe	Gln	Ile	Gln	245	250	255	
Ser	Ala	Leu	Lys	Leu	Ala	Ile	Tyr	Lys	Ala	Thr	Asn	Leu	Val	Pro	Thr	260	265	270	
Ser	Thr	Phe	Leu	Leu	His	Ser	Asp	Phe	Glu	Gln	Val	Thr	Cys	Ile	Lys	275	280	285	
Glu	Asn	Lys	Ile	Val	Lys	Leu	Leu	Leu	Cys	Gln	Asn	Tyr	Asp	Pro	Leu	290	295	300	
Leu	Val	Gly	Gln	His	Val	Leu	Arg	Trp	Ile	Asp	Lys	Lys	Cys	Gly	Lys	305	310	315	320

Lys Asn Thr Leu Trp Phe Tyr Gly Pro Pro Ser Thr Gly Lys Thr Asn  
 325 330 335  
 Leu Ala Met Ala Ile Ala Lys Thr Val Pro Val Tyr Gly Met Val Asn  
 340 345 350  
 Trp Asn Asn Glu Asn Phe Pro Phe Asn Asp Val Ala Gly Lys Ser Leu  
 355 360 365  
 Val Val Trp Asp Glu Gly Ile Ile Lys Ser Thr Ile Val Glu Ala Ala  
 370 375 380  
 Lys Ala Ile Leu Gly Gly Gln Pro Thr Arg Val Asp Gln Lys Met Arg  
 385 390 395 400  
 Gly Ser Val Ala Val Pro Gly Val Pro Val Val Ile Thr Ser Asn Gly  
 405 410 415  
 Asp Ile Thr Phe Val Val Ser Gly Asn Thr Thr Thr Thr Val His Ala  
 420 425 430  
 Lys Ala Leu Lys Glu Arg Met Val Lys Leu Asn Phe Thr Ile Arg Cys  
 435 440 445  
 Ser Pro Asp Met Gly Leu Leu Thr Glu Ala Asp Val Gln Gln Trp Leu  
 450 455 460  
 Thr Trp Cys Asn Ala Gln Ser Trp Ser His Tyr Glu Asn Trp Ala Ile  
 465 470 475 480  
 Asn Tyr Thr Phe Asp Phe Pro Gly Ile Asn Ala Asp Ala Leu His Pro  
 485 490 495  
 Asp Leu Gln Thr Thr Pro Ile Val Pro Asp Thr Ser Ile Ser Ser Ser  
 500 505 510  
 Gly Gly Glu Ser Ser Glu Glu Leu Ser Glu Ser Ser Phe Phe Asn Leu  
 515 520 525  
 Ile Thr Pro Gly Ala Trp Asn Ser Glu Thr Pro Arg Ser Ser Thr Pro  
 530 535 540  
 Val Pro Gly Thr Ser Ser Gly Glu Ser Phe Val Gly Ser Pro Val Ser  
 545 550 555 560  
 Ser Glu Val Val Ala Ala Ser Trp Glu Glu Ala Phe Tyr Thr Pro Leu  
 565 570 575  
 Ala Asp Gln Phe Arg Glu Leu Leu Val Gly Val Asp Phe Val Trp Asp  
 580 585 590  
 Gly Val Arg Gly Leu Pro Val Cys Cys Val Glu His Ile Asn Asn Ser  
 595 600 605  
 Gly Gly Gly Leu Gly Leu Cys Pro His Cys Ile Asn Val Gly Ala Trp  
 610 615 620

Tyr Asn Gly Trp Lys Phe Arg Glu Phe Thr Pro Asp Leu Val Arg Cys  
625 630 635 640

Ser Cys His Val Gly Ala Ser Asn Pro Phe Ser Val Leu Thr Cys Lys  
645 650 655

Lys Cys Ala Tyr Leu Ser Gly Leu Gln Ser Phe Val Asp Tyr Glu  
660 665 670

<210> 83

<211> 222

<212> DNA

<213> erythrovirus

<400> 83

atg cag atg ccc tcc acc cag atc tcc aaa cca ccc cca ttg tcc cag 48  
Met Gln Met Pro Ser Thr Gln Ile Ser Lys Pro Pro Pro Leu Ser Gln  
675 680 685

aca cca gta tca gca gca gtg gtg gtg aaa gct ctg aag aac tca gtg 96  
Thr Pro Val Ser Ala Ala Val Val Lys Ala Leu Lys Asn Ser Val  
690 695 700

aaa gca gct ttt tca acc tca tca ctc cag gcg cct gga aca gtg aaa 144  
Lys Ala Ala Phe Ser Thr Ser Ser Leu Gln Ala Pro Gly Thr Val Lys  
705 710 715

ccc cgc gct cta gta cgc ccg tcc ccg gga cca gtt cag gag aat cat 192  
Pro Arg Ala Leu Val Arg Pro Ser Pro Gly Pro Val Gln Glu Asn His  
720 725 730 735

ttg tcg gaa gcc cag ttt cct ccg aag tgg 222  
Leu Ser Glu Ala Gln Phe Pro Pro Lys Trp  
740 745

<210> 84

<211> 74

<212> PRT

<213> erythrovirus

<400> 84

Met Gln Met Pro Ser Thr Gln Ile Ser Lys Pro Pro Pro Leu Ser Gln  
1 5 10 15

Thr Pro Val Ser Ala Ala Val Val Val Lys Ala Leu Lys Asn Ser Val  
20 25 30

Lys Ala Ala Phe Ser Thr Ser Ser Leu Gln Ala Pro Gly Thr Val Lys  
35 40 45

Pro Arg Ala Leu Val Arg Pro Ser Pro Gly Pro Val Gln Glu Asn His  
50 55 60

Leu Ser Glu Ala Gln Phe Pro Pro Lys Trp  
65 70

<210> 85

<211> 2343

<212> DNA

## &lt;213&gt; erythrovirus

&lt;400&gt; 85

atg agt aaa acc act aac aaa tgg tgg gaa agc agt gac aaa ttt gcc	48
Met Ser Lys Thr Thr Asn Lys Trp Trp Glu Ser Ser Asp Lys Phe Ala	
75 80 85 90	
cag gac gtg tat aag cag ttt gtg caa ttt tat gaa aaa gct act gga	96
Gln Asp Val Tyr Lys Gln Phe Val Gln Phe Tyr Glu Lys Ala Thr Gly	
95 100 105	
aca gac tta gag ctt att caa att tta aaa gac cat tac aac att tct	144
Thr Asp Leu Glu Leu Ile Gln Ile Leu Lys Asp His Tyr Asn Ile Ser	
110 115 120	
tta gat aat cct tta gaa aac ccc tct tct tta ttt gac tta gtt gct	192
Leu Asp Asn Pro Leu Glu Asn Pro Ser Ser Leu Phe Asp Leu Val Ala	
125 130 135	
cgc att aaa agt aat ctt aaa aac tct cca gac cta tat agt cat cat	240
Arg Ile Lys Ser Asn Leu Lys Asn Ser Pro Asp Leu Tyr Ser His His	
140 145 150	
ttt cag agc cat gga cag tta tct gac cac ccc cat gcc tta tca tcc	288
Phe Gln Ser His Gly Gln Leu Ser Asp His Pro His Ala Leu Ser Ser	
155 160 165 170	
agt aac agt agt gca gaa cct aga gga gaa aat gca gta tta tct agt	336
Ser Asn Ser Ser Ala Glu Pro Arg Gly Glu Asn Ala Val Leu Ser Ser	
175 180 185	
gaa gac tta cac aag cct ggg caa gtt agc ata caa tta ccc ggt act	384
Glu Asp Leu His Lys Pro Gly Gln Val Ser Ile Gln Leu Pro Gly Thr	
190 195 200	
aac tat gtt ggg cct ggc aat gag cta caa gct ggg cct ccg cag aat	432
Asn Tyr Val Gly Pro Gly Asn Glu Leu Gln Ala Gly Pro Pro Gln Asn	
205 210 215	
gct gtg gac agt gct gca agg att cat gac ttt agg tat agc caa ttg	480
Ala Val Asp Ser Ala Ala Arg Ile His Asp Phe Arg Tyr Ser Gln Leu	
220 225 230	
gct aag ttg gga ata aat cct tat aca cat tgg acg gta gca gat gaa	528
Ala Lys Leu Gly Ile Asn Pro Tyr Thr His Trp Thr Val Ala Asp Glu	
235 240 245 250	
gaa ttg tta aaa aat ata aaa aat gaa aca ggg ttt caa gca caa gca	576
Glu Leu Leu Lys Asn Ile Lys Asn Glu Thr Gly Phe Gln Ala Gln Ala	
255 260 265	
gta aaa gat tac ttt act tta aaa ggt gca gct gcc cct gtg gcc cat	624
Val Lys Asp Tyr Phe Thr Leu Lys Gly Ala Ala Ala Pro Val Ala His	
270 275 280	
ttt caa gga agt tta ccg gaa gtg ccc gcg tac aac gcc tca gaa aaa	672
Phe Gln Gly Ser Leu Pro Glu Val Pro Ala Tyr Asn Ala Ser Glu Lys	
285 290 295	

tac ccc agc atg act tca gtt aac tct gca gaa gcc agc act ggt gca Tyr Pro Ser Met Thr Ser Val Asn Ser Ala Glu Ala Ser Thr Gly Ala 300 305 310	720
ggc ggg gga ggt agc aac cct aca aaa agc atg tgg agt gaa ggg gct Gly Gly Gly Gly Ser Asn Pro Thr Lys Ser Met Trp Ser Glu Gly Ala 315 320 325 330	768
aca ttt act gct aat tct gta acg tgt aca ttc tct agg caa ttt tta Thr Phe Thr Ala Asn Ser Val Thr Cys Thr Phe Ser Arg Gln Phe Leu 335 340 345	816
att cca tat gat cca gag cat cat tat aaa gtg ttc tct cca gca gct Ile Pro Tyr Asp Pro Glu His His Tyr Lys Val Phe Ser Pro Ala Ala 350 355 360	864
agt agc tgc cac aat gct agt ggg aaa gag gca aaa gtg tgc act att Ser Ser Cys His Asn Ala Ser Gly Lys Glu Ala Lys Val Cys Thr Ile 365 370 375	912
agt ccc att atg ggg tac tct act ccg tgg aga tac tta gat ttt aat Ser Pro Ile Met Gly Tyr Ser Thr Pro Trp Arg Tyr Leu Asp Phe Asn 380 385 390	960
gct tta aat ttg ttt ttc tca cca tta gag ttt cag cac tta att gaa Ala Leu Asn Leu Phe Phe Ser Pro Leu Glu Phe Gln His Leu Ile Glu 395 400 405 410	1008
aat tat ggt agt ata gct cca gat gct tta act gta act att tca gaa Asn Tyr Gly Ser Ile Ala Pro Asp Ala Leu Thr Val Thr Ile Ser Glu 415 420 425	1056
att gct gta aaa gat gtc aca gac aaa aca gga gga ggt gtg caa gtt Ile Ala Val Lys Asp Val Thr Asp Lys Thr Gly Gly Gly Val Gln Val 430 435 440	1104
act gac agc acc aca gga cgt ttg tgt atg tta gtg gat cat gag tat Thr Asp Ser Thr Thr Gly Arg Leu Cys Met Leu Val Asp His Glu Tyr 445 450 455	1152
aaa tac cca tat gtg cta ggt cag gga caa gac aca cta gct cca gaa Lys Tyr Pro Tyr Val Leu Gly Gln Gly Gln Asp Thr Leu Ala Pro Glu 460 465 470	1200
ctg ccc att tgg gtt tac ttt ccc ccc cag tat gct tac tta aca gta Leu Pro Ile Trp Val Tyr Phe Pro Pro Gln Tyr Ala Tyr Leu Thr Val 475 480 485 490	1248
ggt gaa gta aac aca caa gga att tca gga gac agc aaa aaa ttg gct Gly Glu Val Asn Thr Gln Gly Ile Ser Gly Asp Ser Lys Lys Leu Ala 495 500 505	1296
agt gaa gaa tca gct ttt tat gtg tta gag cac agt tca ttt gaa ctt Ser Glu Glu Ser Ala Phe Tyr Val Leu Glu His Ser Ser Phe Glu Leu 510 515 520	1344
ttg ggt aca ggg gga tct gcc act atg tcc tac aaa ttt cca gct gtg Leu Gly Thr Gly Gly Ser Ala Thr Met Ser Tyr Lys Phe Pro Ala Val 525 530 535	1392



ccc cca gaa aac cta gaa ggc tgc agc caa cat ttt tat gaa atg tac	1440
Pro Pro Glu Asn Leu Glu Gly Cys Ser Gln His Phe Tyr Glu Met Tyr	
540 545 550	
aac cct ttg tac ggt tct cgt tta ggg gta cct gac aca tta gga ggg	1488
Asn Pro Leu Tyr Gly Ser Arg Leu Gly Val Pro Asp Thr Leu Gly Gly	
555 560 565 570	
gac cct aaa ttt aga tca ttg aca cac gaa gac cac gca att cag cca	1536
Asp Pro Lys Phe Arg Ser Leu Thr His Glu Asp His Ala Ile Gln Pro	
575 580 585	
caa aac ttt atg cct ggg cca cta ata aat tca gtg tct acc aaa gaa	1584
Gln Asn Phe Met Pro Gly Pro Leu Ile Asn Ser Val Ser Thr Lys Glu	
590 595 600	
gga gac aat tct aat aca ggt gct gga aaa gcc ctt acg ggg ctt agt	1632
Gly Asp Asn Ser Asn Thr Gly Ala Gly Lys Ala Leu Thr Gly Leu Ser	
605 610 615	
act ggc act agc caa aac acc aga att tcc cta cgc ccc ggg cca gta	1680
Thr Gly Thr Ser Gln Asn Thr Arg Ile Ser Leu Arg Pro Gly Pro Val	
620 625 630	
tct cag cca tac cat cac tgg gac act gat aaa tat gtt aca gga ata	1728
Ser Gln Pro Tyr His His Trp Asp Thr Asp Lys Tyr Val Thr Gly Ile	
635 640 645 650	
aat gcc att tca cat gga caa acc act tat gga aat gct gag gac aaa	1776
Asn Ala Ile Ser His Gly Gln Thr Thr Tyr Gly Asn Ala Glu Asp Lys	
655 660 665	
gag tat cag caa ggg gta gga aga ttt cca aat gaa aaa gaa cag ctt	1824
Glu Tyr Gln Gln Gly Val Gly Arg Phe Pro Asn Glu Lys Glu Gln Leu	
670 675 680	
aag cag tta caa ggt ctt aac atg cac aca tac ttc cct aat aaa gga	1872
Lys Gln Leu Gln Gly Leu Asn Met His Thr Tyr Phe Pro Asn Lys Gly	
685 690 695	
acc caa caa tac aca gac caa att gaa cgc cct ctt atg gtg ggc tct	1920
Thr Gln Gln Tyr Thr Asp Gln Ile Glu Arg Pro Leu Met Val Gly Ser	
700 705 710	
gtt tgg aac aga aga gct ctt cac tat gaa agt cag ctg tgg agt aaa	1968
Val Trp Asn Arg Arg Ala Leu His Tyr Glu Ser Gln Leu Trp Ser Lys	
715 720 725 730	
atc cct aac tta gat gac agt ttt aaa act caa ttt gca gcc cta ggc	2016
Ile Pro Asn Leu Asp Asp Ser Phe Lys Thr Gln Phe Ala Ala Leu Gly	
735 740 745	
ggg tgg ggt ttg cat caa cca ccc cct caa ata ttt tta aaa ata cta	2064
Gly Trp Gly Leu His Gln Pro Pro Gln Ile Phe Leu Lys Ile Leu	
750 755 760	

Ala Val Asp Ser Ala Ala Arg Ile His Asp Phe Arg Tyr Ser Gln Leu  
145 150 155 160

Ala Lys Leu Gly Ile Asn Pro Tyr Thr His Trp Thr Val Ala Asp Glu  
 165 170 175  
 Glu Leu Leu Lys Asn Ile Lys Asn Glu Thr Gly Phe Gln Ala Gln Ala  
 180 185 190  
 Val Lys Asp Tyr Phe Thr Leu Lys Gly Ala Ala Ala Pro Val Ala His  
 195 200 205  
 Phe Gln Gly Ser Leu Pro Glu Val Pro Ala Tyr Asn Ala Ser Glu Lys  
 210 215 220  
 Tyr Pro Ser Met Thr Ser Val Asn Ser Ala Glu Ala Ser Thr Gly Ala  
 225 230 235 240  
 Gly Gly Gly Gly Ser Asn Pro Thr Lys Ser Met Trp Ser Glu Gly Ala  
 245 250 255  
 Thr Phe Thr Ala Asn Ser Val Thr Cys Thr Phe Ser Arg Gln Phe Leu  
 260 265 270  
 Ile Pro Tyr Asp Pro Glu His His Tyr Lys Val Phe Ser Pro Ala Ala  
 275 280 285  
 Ser Ser Cys His Asn Ala Ser Gly Lys Glu Ala Lys Val Cys Thr Ile  
 290 295 300  
 Ser Pro Ile Met Gly Tyr Ser Thr Pro Trp Arg Tyr Leu Asp Phe Asn  
 305 310 315 320  
 Ala Leu Asn Leu Phe Phe Ser Pro Leu Glu Phe Gln His Leu Ile Glu  
 325 330 335  
 Asn Tyr Gly Ser Ile Ala Pro Asp Ala Leu Thr Val Thr Ile Ser Glu  
 340 345 350  
 Ile Ala Val Lys Asp Val Thr Asp Lys Thr Gly Gly Gly Val Gln Val  
 355 360 365  
 Thr Asp Ser Thr Thr Gly Arg Leu Cys Met Leu Val Asp His Glu Tyr  
 370 375 380  
 Lys Tyr Pro Tyr Val Leu Gly Gln Gly Gln Asp Thr Leu Ala Pro Glu  
 385 390 395 400  
 Leu Pro Ile Trp Val Tyr Phe Pro Pro Gln Tyr Ala Tyr Leu Thr Val  
 405 410 415  
 Gly Glu Val Asn Thr Gln Gly Ile Ser Gly Asp Ser Lys Lys Leu Ala  
 420 425 430  
 Ser Glu Glu Ser Ala Phe Tyr Val Leu Glu His Ser Ser Phe Glu Leu  
 435 440 445  
 Leu Gly Thr Gly Gly Ser Ala Thr Met Ser Tyr Lys Phe Pro Ala Val  
 450 455 460

Pro Pro Glu Asn Leu Glu Gly Cys Ser Gln His Phe Tyr Glu Met Tyr  
 465 470 475 480  
 Asn Pro Leu Tyr Gly Ser Arg Leu Gly Val Pro Asp Thr Leu Gly Gly  
 485 490 495  
 Asp Pro Lys Phe Arg Ser Leu Thr His Glu Asp His Ala Ile Gln Pro  
 500 505 510  
 Gln Asn Phe Met Pro Gly Pro Leu Ile Asn Ser Val Ser Thr Lys Glu  
 515 520 525  
 Gly Asp Asn Ser Asn Thr Gly Ala Gly Lys Ala Leu Thr Gly Leu Ser  
 530 535 540  
 Thr Gly Thr Ser Gln Asn Thr Arg Ile Ser Leu Arg Pro Gly Pro Val  
 545 550 555 560  
 Ser Gln Pro Tyr His His Trp Asp Thr Asp Lys Tyr Val Thr Gly Ile  
 565 570 575  
 Asn Ala Ile Ser His Gly Gln Thr Thr Tyr Gly Asn Ala Glu Asp Lys  
 580 585 590  
 Glu Tyr Gln Gln Gly Val Gly Arg Phe Pro Asn Glu Lys Glu Gln Leu  
 595 600 605  
 Lys Gln Leu Gln Gly Leu Asn Met His Thr Tyr Phe Pro Asn Lys Gly  
 610 615 620  
 Thr Gln Gln Tyr Thr Asp Gln Ile Glu Arg Pro Leu Met Val Gly Ser  
 625 630 635 640  
 Val Trp Asn Arg Arg Ala Leu His Tyr Glu Ser Gln Leu Trp Ser Lys  
 645 650 655  
 Ile Pro Asn Leu Asp Asp Ser Phe Lys Thr Gln Phe Ala Ala Leu Gly  
 660 665 670  
 Gly Trp Gly Leu His Gln Pro Pro Pro Gln Ile Phe Leu Lys Ile Leu  
 675 680 685  
 Pro Gln Ser Gly Pro Ile Gly Gly Ile Lys Ser Met Gly Ile Thr Thr  
 690 695 700  
 Leu Val Gln Tyr Ala Val Gly Ile Met Thr Val Thr Met Thr Phe Lys  
 705 710 715 720  
 Leu Gly Pro Arg Lys Ala Thr Gly Arg Trp Asn Pro Gln Pro Gly Val  
 725 730 735  
 Tyr Pro Pro His Ala Ala Gly His Leu Pro Tyr Val Leu Tyr Asp Pro  
 740 745 750  
 Thr Ala Thr Asp Ala Lys Gln His Arg His Gly Tyr Glu Lys Pro  
 755 760 765  
 Glu Glu Leu Trp Thr Ala Lys Ser Arg Val His Pro Leu  
 770 775 780

<210> 87  
 <211> 681  
 <212> DNA  
 <213> erythrovirus

<400> 87

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Met Ser Lys Thr Thr Asn Lys Trp Trp Glu Ser Ser Asp Lys Phe Ala	
785 790 795	
cag gac gtg tat aag cag ttt gtg caa ttt tat gaa aaa gct act gga	96
Gln Asp Val Tyr Lys Gln Phe Val Gln Phe Tyr Glu Lys Ala Thr Gly	
800 805 810	
aca gac tta gag ctt att caa att tta aaa gac cat tac aac att tct	144
Thr Asp Leu Glu Leu Ile Gln Ile Leu Lys Asp His Tyr Asn Ile Ser	
815 820 825	
tta gat aat cct tta gaa aac ccc tct tct tta ttt gac tta gtt gct	192
Leu Asp Asn Pro Leu Glu Asn Pro Ser Ser Leu Phe Asp Leu Val Ala	
830 835 840 845	
cgc att aaa agt aat ctt aaa aac tct cca gac cta tat agt cat cat	240
Arg Ile Lys Ser Asn Leu Lys Asn Ser Pro Asp Leu Tyr Ser His His	
850 855 860	
ttt cag agc cat gga cag tta tct gac cac ccc cat gcc tta tca tcc	288
Phe Gln Ser His Gly Gln Leu Ser Asp His Pro His Ala Leu Ser Ser	
865 870 875	
agt aac agt agt gca gaa cct aga gga gaa aat gca gta tta tct agt	336
Ser Asn Ser Ser Ala Glu Pro Arg Gly Glu Asn Ala Val Leu Ser Ser	
880 885 890	
gaa gac tta cac aag cct ggg caa gtt agc ata caa tta ccc ggt act	384
Glu Asp Leu His Lys Pro Gly Gln Val Ser Ile Gln Leu Pro Gly Thr	
895 900 905	
aac tat gtt ggg cct ggc aat gag cta caa gct ggg cct ccg cag aat	432
Asn Tyr Val Gly Pro Gly Asn Glu Leu Gln Ala Gly Pro Pro Gln Asn	
910 915 920 925	
gct gtg gac agt gct gca agg att cat gac ttt agg tat agc caa ttg	480
Ala Val Asp Ser Ala Ala Arg Ile His Asp Phe Arg Tyr Ser Gln Leu	
930 935 940	
gct aag ttg gga ata aat cct tat aca cat tgg acg gta gca gat gaa	528
Ala Lys Leu Gly Ile Asn Pro Tyr Thr His Trp Thr Val Ala Asp Glu	
945 950 955	
gaa ttg tta aaa aat ata aaa aat gaa aca ggg ttt caa gca caa gca	576
Glu Leu Leu Lys Asn Ile Lys Asn Glu Thr Gly Phe Gln Ala Gln Ala	
960 965 970	
gta aaa gat tac ttt act tta aaa ggt gca gct gcc cct gtg gcc cat	624
Val Lys Asp Tyr Phe Thr Leu Lys Gly Ala Ala Pro Val Ala His	
975 980 985	

ttt caa gga agt tta ccg gaa gtg ccc gcg tac aac gcc tca gaa aaa 672  
 Phe Gln Gly Ser Leu Pro Glu Val Pro Ala Tyr Asn Ala Ser Glu Lys  
 990 995 1000 1005

tac ccc agc 681  
 Tyr Pro Ser

<210> 88  
 <211> 227  
 <212> PRT  
 <213> erythrovirus

<400> 88  
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 Gln Asp Val Tyr Lys Gln Phe Val Gln Phe Tyr Glu Lys Ala Thr Gly  
 20 25 30  
 Thr Asp Leu Glu Leu Ile Gln Ile Leu Lys Asp His Tyr Asn Ile Ser  
 35 40 45  
 Leu Asp Asn Pro Leu Glu Asn Pro Ser Ser Leu Phe Asp Leu Val Ala  
 50 55 60  
 Arg Ile Lys Ser Asn Leu Lys Asn Ser Pro Asp Leu Tyr Ser His His  
 65 70 75 80  
 Phe Gln Ser His Gly Gln Leu Ser Asp His Pro His Ala Leu Ser Ser  
 85 90 95  
 Ser Asn Ser Ser Ala Glu Pro Arg Gly Glu Asn Ala Val Leu Ser Ser  
 100 105 110  
 Glu Asp Leu His Lys Pro Gly Gln Val Ser Ile Gln Leu Pro Gly Thr  
 115 120 125  
 Asn Tyr Val Gly Pro Gly Asn Glu Leu Gln Ala Gly Pro Pro Gln Asn  
 130 135 140  
 Ala Val Asp Ser Ala Ala Arg Ile His Asp Phe Arg Tyr Ser Gln Leu  
 145 150 155 160  
 Ala Lys Leu Gly Ile Asn Pro Tyr Thr His Trp Thr Val Ala Asp Glu  
 165 170 175  
 Glu Leu Leu Lys Asn Ile Lys Asn Glu Thr Gly Phe Gln Ala Gln Ala  
 180 185 190  
 Val Lys Asp Tyr Phe Thr Leu Lys Gly Ala Ala Ala Pro Val Ala His  
 195 200 205  
 Phe Gln Gly Ser Leu Pro Glu Val Pro Ala Tyr Asn Ala Ser Glu Lys  
 210 215 220  
 Tyr Pro Ser  
 225

<210> 89  
 <211> 306  
 <212> DNA  
 <213> erythrovirus

<400> 89  
 ttg ctc gca tta aaa gta atc tta aaa act ctc cag acc tat ata gtc 48  
 Leu Leu Ala Leu Lys Val Ile Leu Lys Thr Leu Gln Thr Tyr Ile Val  
           230                  235                  240

atc att ttc aga gcc atg gac agt tat ctg acc acc ccc atg cct tat 96  
 Ile Ile Phe Arg Ala Met Asp Ser Tyr Leu Thr Thr Pro Met Pro Tyr  
           245                  250                  255

cat cca gta aca gta gtg cag aac cta gag gag aaa atg cag tat tat 144  
 His Pro Val Thr Val Val Gln Asn Leu Glu Glu Lys Met Gln Tyr Tyr  
 260                  265                  270                  275

cta gtg aag act tac aca agc ctg ggc aag tta gca tac aat tac ccg 192  
 Leu Val Lys Thr Tyr Thr Ser Leu Gly Lys Leu Ala Tyr Asn Tyr Pro  
                           280                  285                  290

gta cta act atg ttg ggc ctg gca atg agc tac aag ctg ggc ctc cgc 240  
 Val Leu Thr Met Leu Gly Leu Ala Met Ser Tyr Lys Leu Gly Leu Arg  
                   295                  300                  305

aga atg ctg tgg aca gtg ctg caa gga ttc atg act tta ggt ata gcc 288  
 Arg Met Leu Trp Thr Val Leu Gln Gly Phe Met Thr Leu Gly Ile Ala  
           310                  315                  320

aat tgg cta agt tgg gaa 306  
 Asn Trp Leu Ser Trp Glu  
           325

<210> 90  
 <211> 102  
 <212> PRT  
 <213> erythrovirus

<400> 90  
 Leu Leu Ala Leu Lys Val Ile Leu Lys Thr Leu Gln Thr Tyr Ile Val  
   1                  5                  10                  15

Ile Ile Phe Arg Ala Met Asp Ser Tyr Leu Thr Thr Pro Met Pro Tyr  
           20                  25                  30

His Pro Val Thr Val Val Gln Asn Leu Glu Glu Lys Met Gln Tyr Tyr  
           35                  40                  45

Leu Val Lys Thr Tyr Thr Ser Leu Gly Lys Leu Ala Tyr Asn Tyr Pro  
   50                  55                  60

Val Leu Thr Met Leu Gly Leu Ala Met Ser Tyr Lys Leu Gly Leu Arg  
   65                  70                  75                  80

Arg Met Leu Trp Thr Val Leu Gln Gly Phe Met Thr Leu Gly Ile Ala  
           85                  90                  95

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<210> 91
<211> 1662
<212> DNA
<213> erythrovirus
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atg act tca gtt aac tct gca gaa gcc agc act ggt gca ggc ggg gga 48  
Met Thr Ser Val Asn Ser Ala Glu Ala Ser Thr Gly Ala Gly Gly Gly  
105 110 115

ggt agc aac cct aca aaa agc atg tgg agt gaa ggg gct aca ttt act 96  
 Gly Ser Asn Pro Thr Lys Ser Met Trp Ser Glu Gly Ala Thr Phe Thr  
 120 125 130

gct aat tct gta acg tgt aca ttc tct agg caa ttt tta att cca tat 144  
Ala Asn Ser Val Thr Cys Thr Phe Ser Arg Gln Phe Leu Ile Pro Tyr  
135 140 145 150

gat cca gag cat cat tat aaa gtg ttc tct cca gca gct agt agc tgc 192  
Asp Pro Glu His His Tyr Lys Val Phe Ser Pro Ala Ala Ser Ser Cys  
155 160 165

cac aat gct agt ggg aaa gag gca aaa gtg tgc act att agt ccc att 240  
 His Asn Ala Ser Gly Lys Glu Ala Lys Val Cys Thr Ile Ser Pro Ile  
 170 175 180

atg ggg tac tct act ccg tgg aga tac tta gat ttt aat gct tta aat 288  
Met Gly Tyr Ser Thr Pro Trp Arg Tyr Leu Asp Phe Asn Ala Leu Asn  
185 190 195

ttg ttt ttc tca cca tta gag ttt cag cac tta att gaa aat tat ggt 336  
Leu Phe Phe Ser Pro Leu Glu Phe Gln His Leu Ile Glu Asn Tyr Gly  
200 205 210

agt ata gct cca gat gct tta act gta act att tca gaa att gct gta 384  
Ser Ile Ala Pro Asp Ala Leu Thr Val Thr Ile Ser Glu Ile Ala Val  
215 220 225 230

aaa gat gtc aca gac aaa aca gga gga ggt gtg caa gtt act gac agc 432  
Lys Asp Val Thr Asp Lys Thr Gly Gly Gly Val Gln Val Thr Asp Ser  
235 240 245

acc aca gga cgt ttg tgt atg tta gtg gat cat gag tat aaa tac cca 480  
Thr Thr Gly Arg Leu Cys Met Leu Val Asp His Glu Tyr Lys Tyr Pro  
250 255 260

tat	gtg	cta	ggt	cag	gga	caa	gac	aca	cta	gct	cca	gaa	ctg	ccg	att	528
Tyr	Val	Leu	Gly	Gln	Gly	Gln	Asp	Thr	Leu	Ala	Pro	Glu	Leu	Pro	Ile	
		265					270					275				

tgg gtt tac ttt ccc ccc cag tat gct tac tta aca gta ggt gaa gta 576  
Trp Val Tyr Phe Pro Pro Gln Tyr Ala Tyr Leu Thr Val Gly Glu Val  
280 285 290



aac aca caa gga att tca gga gac agc aaa aaa ttg gct agt gaa gaa	624
Asn Thr Gln Gly Ile Ser Gly Asp Ser Lys Lys Leu Ala Ser Glu Glu	
295 300 305 310	
tca gct ttt tat gtg tta gag cac agt tca ttt gaa ctt ttg ggt aca	672
Ser Ala Phe Tyr Val Leu Glu His Ser Ser Phe Glu Leu Leu Gly Thr	
315 320 325	
ggg gga tct gcc act atg tcc tac aaa ttt cca gct gtg ccc cca gaa	720
Gly Gly Ser Ala Thr Met Ser Tyr Lys Phe Pro Ala Val Pro Pro Glu	
330 335 340	
aac cta gaa ggc tgc agc caa cat ttt tat gaa atg tac aac cct ttg	768
Asn Leu Glu Gly Cys Ser Gln His Phe Tyr Glu Met Tyr Asn Pro Leu	
345 350 355	
tac ggt tct cgt tta ggg gta cct gac aca tta gga ggg gac cct aaa	816
Tyr Gly Ser Arg Leu Gly Val Pro Asp Thr Leu Gly Gly Asp Pro Lys	
360 365 370	
ttt aga tca ttg aca cac gaa gac cac gca att cag cca caa aac ttt	864
Phe Arg Ser Leu Thr His Glu Asp His Ala Ile Gln Pro Gln Asn Phe	
375 380 385 390	
atg cct ggg cca cta ata aat tca gtg tct acc aaa gaa gga gac aat	912
Met Pro Gly Pro Leu Ile Asn Ser Val Ser Thr Lys Glu Gly Asp Asn	
395 400 405	
tct aat aca ggt gct gga aaa gcc ctt acg ggg ctt agt act ggc act	960
Ser Asn Thr Gly Ala Gly Lys Ala Leu Thr Gly Leu Ser Thr Gly Thr	
410 415 420	
agc caa aac acc aga att tcc cta cgc ccc ggg cca gta tct cag cca	1008
Ser Gln Asn Thr Arg Ile Ser Leu Arg Pro Gly Pro Val Ser Gln Pro	
425 430 435	
tac cat cac tgg gac act gat aaa tat gtt aca gga ata aat gcc att	1056
Tyr His His Trp Asp Thr Asp Lys Tyr Val Thr Gly Ile Asn Ala Ile	
440 445 450	
tca cat gga caa acc act tat gga aat gct gag gac aaa gag tat cag	1104
Ser His Gly Gln Thr Thr Tyr Gly Asn Ala Glu Asp Lys Glu Tyr Gln	
455 460 465 470	
caa ggg gta gga aga ttt cca aat gaa aaa gaa cag ctt aag cag tta	1152
Gln Gly Val Gly Arg Phe Pro Asn Glu Lys Glu Gln Leu Lys Gln Leu	
475 480 485	
caa ggt ctt aac atg cac aca tac ttc cct aat aaa gga acc caa caa	1200
Gln Gly Leu Asn Met His Thr Tyr Phe Pro Asn Lys Gly Thr Gln Gln	
490 495 500	
tac aca gac caa att gaa cgc cct ctt atg gtg ggc tct gtt tgg aac	1248
Tyr Thr Asp Gln Ile Glu Arg Pro Leu Met Val Gly Ser Val Trp Asn	
505 510 515	
aga aga gct ctt cac tat gaa agt cag ctg tgg agt aaa atc cct aac	1296
Arg Arg Ala Leu His Tyr Glu Ser Gln Leu Trp Ser Lys Ile Pro Asn	
520 525 530	

tta gat gac agt ttt aaa act caa ttt gca gcc cta ggc ggg tgg ggt 1344  
 Leu Asp Asp Ser Phe Lys Thr Gln Phe Ala Ala Leu Gly Gly Trp Gly  
 535 540 545 550

ttg cat caa cca ccc cct caa ata ttt tta aaa ata cta cca caa agt 1392  
 Leu His Gln Pro Pro Pro Gln Ile Phe Leu Lys Ile Leu Pro Gln Ser  
 555 560 565

ggg cca att gga ggt att aaa tcc atg gga att act act tta gtt caa 1440  
 Gly Pro Ile Gly Gly Ile Lys Ser Met Gly Ile Thr Thr Leu Val Gln  
 570 575 580

tat gct gtg gga ata atg aca gtt acc atg acc ttt aaa ttg gga cct 1488  
 Tyr Ala Val Gly Ile Met Thr Val Thr Met Thr Phe Lys Leu Gly Pro  
 585 590 595

cga aag gct act gga agg tgg aat ccc cag cct ggc gtt tat cct cct 1536  
 Arg Lys Ala Thr Gly Arg Trp Asn Pro Gln Pro Gly Val Tyr Pro Pro  
 600 605 610

cat gca gct ggt cat tta cca tat gta ctg tat gac ccc aca gct aca 1584  
 His Ala Ala Gly His Leu Pro Tyr Val Leu Tyr Asp Pro Thr Ala Thr  
 615 620 625 630

gat gca aag caa cac cac aga cac gga tat gaa aag cct gaa gaa ttg 1632  
 Asp Ala Lys Gln His His Arg His Gly Tyr Glu Lys Pro Glu Glu Leu  
 635 640 645

tgg act gcc aaa agc cgt gtg cac cca ttg 1662  
 Trp Thr Ala Lys Ser Arg Val His Pro Leu  
 650 655

<210> 92

<211> 554

<212> PRT

<213> erythrovirus

<400> 92

Met Thr Ser Val Asn Ser Ala Glu Ala Ser Thr Gly Ala Gly Gly Gly  
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Gly Ser Asn Pro Thr Lys Ser Met Trp Ser Glu Gly Ala Thr Phe Thr  
 20 25 30

Ala Asn Ser Val Thr Cys Thr Phe Ser Arg Gln Phe Leu Ile Pro Tyr  
 35 40 45

Asp Pro Glu His His Tyr Lys Val Phe Ser Pro Ala Ala Ser Ser Cys  
 50 55 60

His Asn Ala Ser Gly Lys Glu Ala Lys Val Cys Thr Ile Ser Pro Ile  
 65 70 75 80

Met Gly Tyr Ser Thr Pro Trp Arg Tyr Leu Asp Phe Asn Ala Leu Asn  
 85 90 95

Leu Phe Phe Ser Pro Leu Glu Phe Gln His Leu Ile Glu Asn Tyr Gly  
 100 105 110

Ser Ile Ala Pro Asp Ala Leu Thr Val Thr Ile Ser Glu Ile Ala Val  
 115 120 125  
 Lys Asp Val Thr Asp Lys Thr Gly Gly Gly Val Gln Val Thr Asp Ser  
 130 135 140  
 Thr Thr Gly Arg Leu Cys Met Leu Val Asp His Glu Tyr Lys Tyr Pro  
 145 150 155 160  
 Tyr Val Leu Gly Gln Gly Gln Asp Thr Leu Ala Pro Glu Leu Pro Ile  
 165 170 175  
 Trp Val Tyr Phe Pro Pro Gln Tyr Ala Tyr Leu Thr Val Gly Glu Val  
 180 185 190  
 Asn Thr Gln Gly Ile Ser Gly Asp Ser Lys Lys Leu Ala Ser Glu Glu  
 195 200 205  
 Ser Ala Phe Tyr Val Leu Glu His Ser Ser Phe Glu Leu Leu Gly Thr  
 210 215 220  
 Gly Gly Ser Ala Thr Met Ser Tyr Lys Phe Pro Ala Val Pro Pro Glu  
 225 230 235 240  
 Asn Leu Glu Gly Cys Ser Gln His Phe Tyr Glu Met Tyr Asn Pro Leu  
 245 250 255  
 Tyr Gly Ser Arg Leu Gly Val Pro Asp Thr Leu Gly Gly Asp Pro Lys  
 260 265 270  
 Phe Arg Ser Leu Thr His Glu Asp His Ala Ile Gln Pro Gln Asn Phe  
 275 280 285  
 Met Pro Gly Pro Leu Ile Asn Ser Val Ser Thr Lys Glu Gly Asp Asn  
 290 295 300  
 Ser Asn Thr Gly Ala Gly Lys Ala Leu Thr Gly Leu Ser Thr Gly Thr  
 305 310 315 320  
 Ser Gln Asn Thr Arg Ile Ser Leu Arg Pro Gly Pro Val Ser Gln Pro  
 325 330 335  
 Tyr His His Trp Asp Thr Asp Lys Tyr Val Thr Gly Ile Asn Ala Ile  
 340 345 350  
 Ser His Gly Gln Thr Thr Tyr Gly Asn Ala Glu Asp Lys Glu Tyr Gln  
 355 360 365  
 Gln Gly Val Gly Arg Phe Pro Asn Glu Lys Glu Gln Leu Lys Gln Leu  
 370 375 380  
 Gln Gly Leu Asn Met His Thr Tyr Phe Pro Asn Lys Gly Thr Gln Gln  
 385 390 395 400  
 Tyr Thr Asp Gln Ile Glu Arg Pro Leu Met Val Gly Ser Val Trp Asn  
 405 410 415

Arg Arg Ala Leu His Tyr Glu Ser Gln Leu Trp Ser Lys Ile Pro Asn  
 420 425 430

Leu Asp Asp Ser Phe Lys Thr Gln Phe Ala Ala Leu Gly Gly Trp Gly  
 435 440 445

Leu His Gln Pro Pro Pro Gln Ile Phe Leu Lys Ile Leu Pro Gln Ser  
 450 455 460

Gly Pro Ile Gly Gly Ile Lys Ser Met Gly Ile Thr Thr Leu Val Gln  
 465 470 475 480

Tyr Ala Val Gly Ile Met Thr Val Thr Met Thr Phe Lys Leu Gly Pro  
 485 490 495

Arg Lys Ala Thr Gly Arg Trp Asn Pro Gln Pro Gly Val Tyr Pro Pro  
 500 505 510

His Ala Ala Gly His Leu Pro Tyr Val Leu Tyr Asp Pro Thr Ala Thr  
 515 520 525

Asp Ala Lys Gln His His Arg His Gly Tyr Glu Lys Pro Glu Glu Leu  
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Trp Thr Ala Lys Ser Arg Val His Pro Leu  
 545 550

<210> 93  
 <211> 396  
 <212> DNA  
 <213> erythrovirus

<400> 93  
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 Pro Leu Asn Trp Asp Leu Glu Arg Leu Leu Glu Gly Gly Ile Pro Ser  
 555 560 565 570

ctg gcg ttt atc ctc ctc atg cag ctg gtc att tac cat atg tac tgt 96  
 Leu Ala Phe Ile Leu Leu Met Gln Leu Val Ile Tyr His Met Tyr Cys  
 575 580 585

atg acc cca cag cta cag atg caa agc aac acc aca gac acg gat atg 144  
 Met Thr Pro Gln Leu Gln Met Gln Ser Asn Thr Thr Asp Thr Asp Met  
 590 595 600

aaa agc ctg aag aat tgt gga ctg cca aaa gcc gtg tgc acc cat tgt 192  
 Lys Ser Leu Lys Asn Cys Gly Leu Pro Lys Ala Val Cys Thr His Cys  
 605 610 615

aaa cat tcc cca ccg tgt cct cag cca gga acc gtc acc cac cgc cca 240  
 Lys His Ser Pro Pro Cys Pro Gln Pro Gly Thr Val Thr His Arg Pro  
 620 625 630

cct gtg ccg ccc aga tta tat gtg ccc cct cca ata ccc cgt agg caa 288  
 Pro Val Pro Pro Arg Leu Tyr Val Pro Pro Pro Ile Pro Arg Arg Gln  
 635 640 645 650

cca tct ata aaa gat aca gac gct gta gaa tat aaa tta tta act aga 336  
 Pro Ser Ile Lys Asp Thr Asp Ala Val Glu Tyr Lys Leu Leu Thr Arg  
                   655                  660                  665

tat gaa caa cat gta att aga atg cta aga tta tgt aat atg tac aca 384  
 Tyr Glu Gln His Val Ile Arg Met Leu Arg Leu Cys Asn Met Tyr Thr  
                   670                  675                  680

agt ttg gaa aaa 396  
 Ser Leu Glu Lys  
                   685

<210> 94  
 <211> 132  
 <212> PRT  
 <213> erythrovirus

<400> 94  
 Pro Leu Asn Trp Asp Leu Glu Arg Leu Leu Glu Gly Gly Ile Pro Ser  
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Leu Ala Phe Ile Leu Leu Met Gln Leu Val Ile Tyr His Met Tyr Cys  
                   20                  25                  30

Met Thr Pro Gln Leu Gln Met Gln Ser Asn Thr Thr Asp Thr Asp Met  
                   35                  40                  45

Lys Ser Leu Lys Asn Cys Gly Leu Pro Lys Ala Val Cys Thr His Cys  
                   50                  55                  60

Lys His Ser Pro Pro Cys Pro Gln Pro Gly Thr Val Thr His Arg Pro  
   65                  70                  75                  80

Pro Val Pro Pro Arg Leu Tyr Val Pro Pro Pro Ile Pro Arg Arg Gln  
                   85                  90                  95

Pro Ser Ile Lys Asp Thr Asp Ala Val Glu Tyr Lys Leu Leu Thr Arg  
                   100                  105                  110

Tyr Glu Gln His Val Ile Arg Met Leu Arg Leu Cys Asn Met Tyr Thr  
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Ser Leu Glu Lys  
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Gln Asp Val Tyr Lys Gln Phe Val Gln Phe Tyr Glu Lys Ala Thr Gly  
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Thr Asp Leu Glu Leu Ile Gln Ile  
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36

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